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Veterinary Faculty
Animal Production Departament

Preliminary genomic analysis for birth weight homogeneity in mice

Abstract no.: 31983

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Animal breeding ➡ **Animal production** ➡ **Productivity Quality Homogeneity**

HOMOGENEITY has been related to:

- ✓ Reduction of the production costs
- ✓ Performance
- ✓ Profitability
- ✓ Animal Welfare
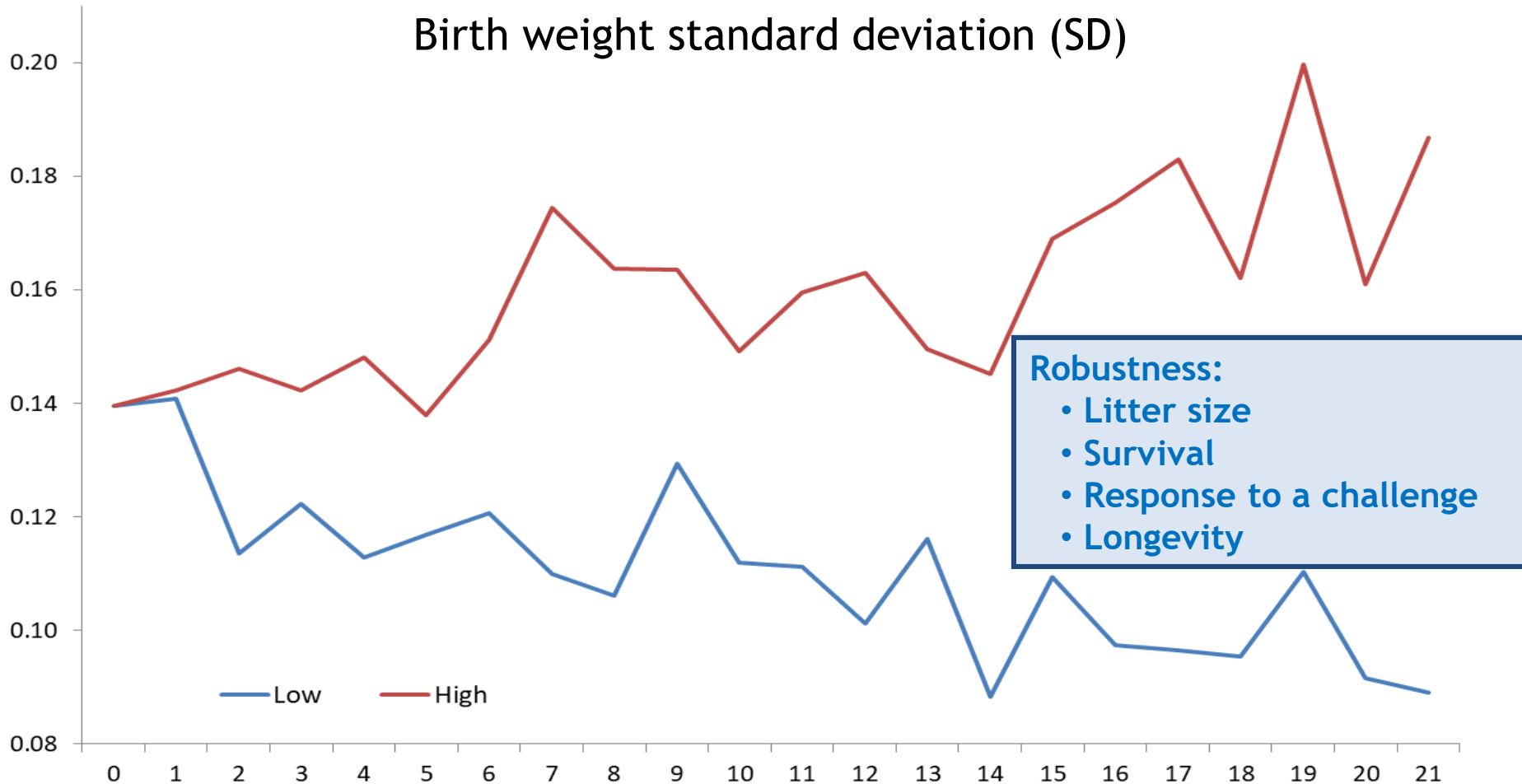- ✓ Efficiency
- ✓ **ROBUSTNESS**

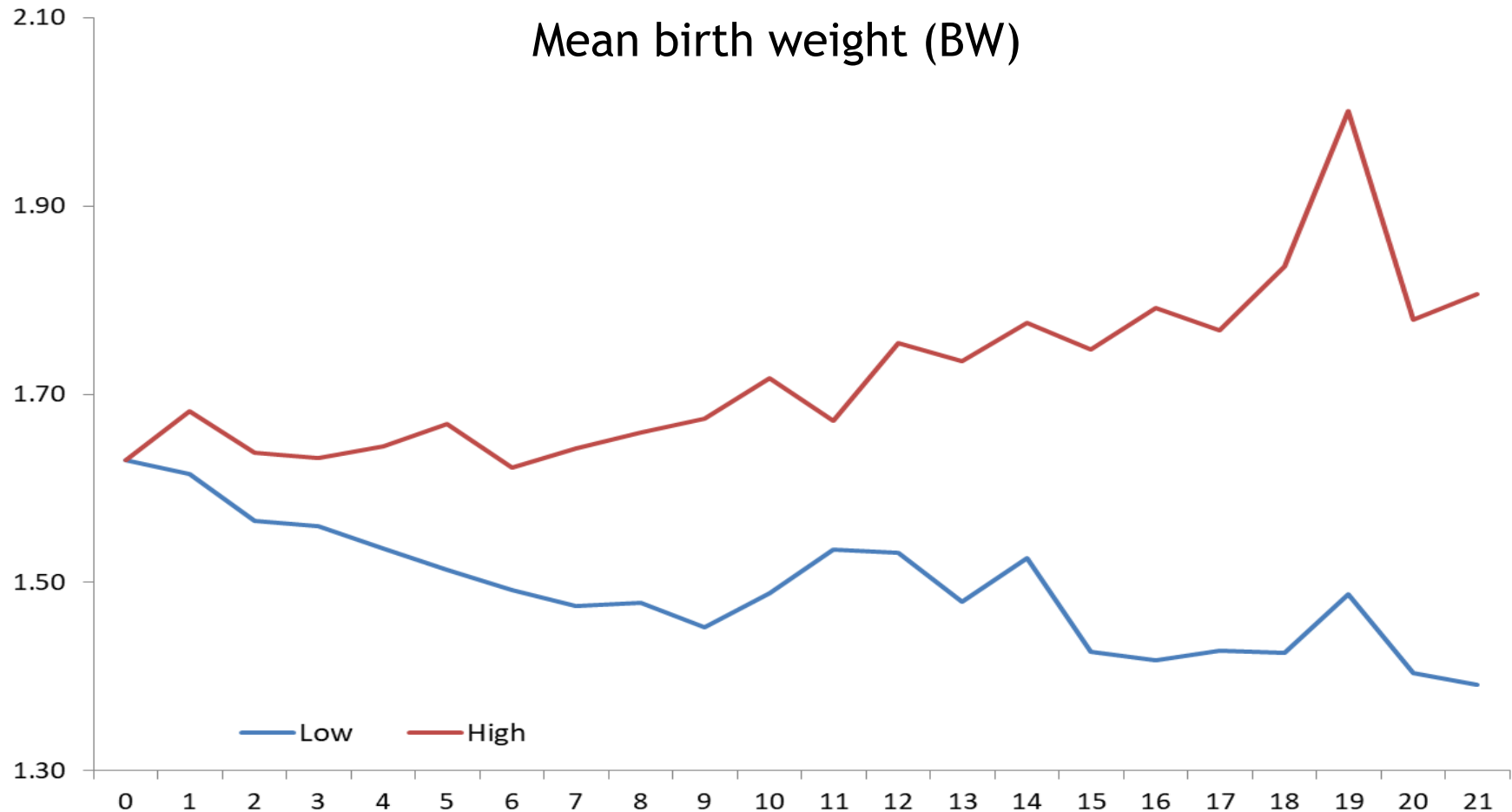Selecting to modify **environmental variability** of some traits has been shown to be possible

Its reduction has been reported to be related to **robustness** with benefits for **animal production** and **welfare**

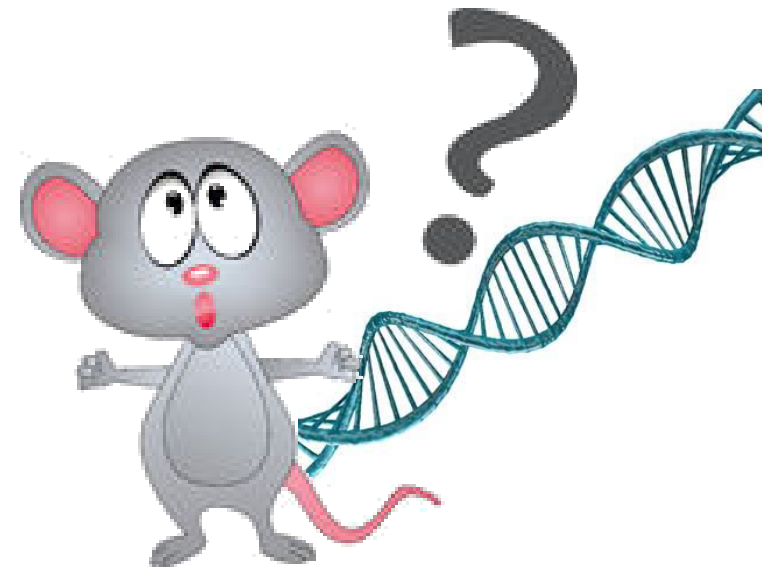# Divergent selection experiment for BIRTH WEIGHT environmental variability

Birth weight standard deviation (SD)

Robustness:
- Litter size
- Survival
- Response to a challenge
- Longevity

Divergent selection experiment for BIRTH WEIGHT environmental variability
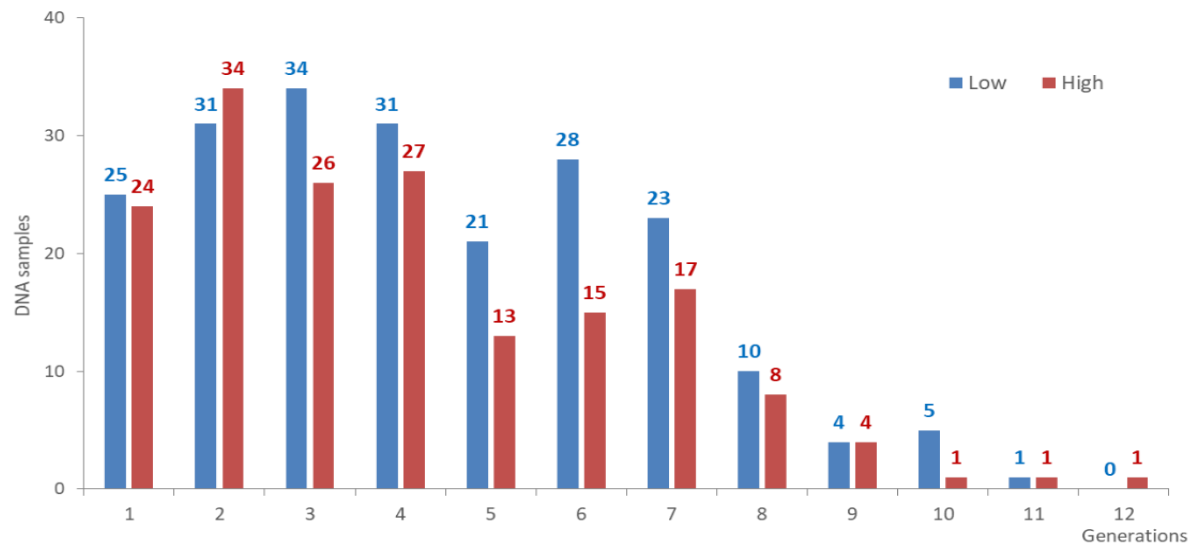

Mean birth weight (BW)

This research aimed at the identification of genomic regions associated to environmental variability for birth weight in mice

PERFORMANCE DATA

Animals proceeded from 20 generations of the divergent selection experiment conducted to modify the environmental variability of BW

384 samples from both lines were choosing by its accuracy

Traits:

✓ Mean birth weight within litter (MBW) in the first parturition

✓ Bith weight standard deviation (SD)

MOLECULAR DATA

384 DNA samples — **212 L-line**

172 H-line

Affymetrix Mouse Diversity Genotyping Array (565,407 SNPs)

Standard quality control:

MAF > 5%

SNPs > 95% animals

Animals > 95% SNPs

189,606 SNPs

METHODS

Model equations:

$$MBW = \mu + Litter\ Size + generation + \sum b_i$$

$$SD = \mu + Litter\ Size + generation + \sum b_i$$

BayesB method: $(\pi = {}^1/_{1000})$ R program (BGLR: Bayesian Generalized Linear Regression)

Markers with effect were selected as those with: $b^2 > 1.1 \cdot 10^{-7}$ a threshold empirically established
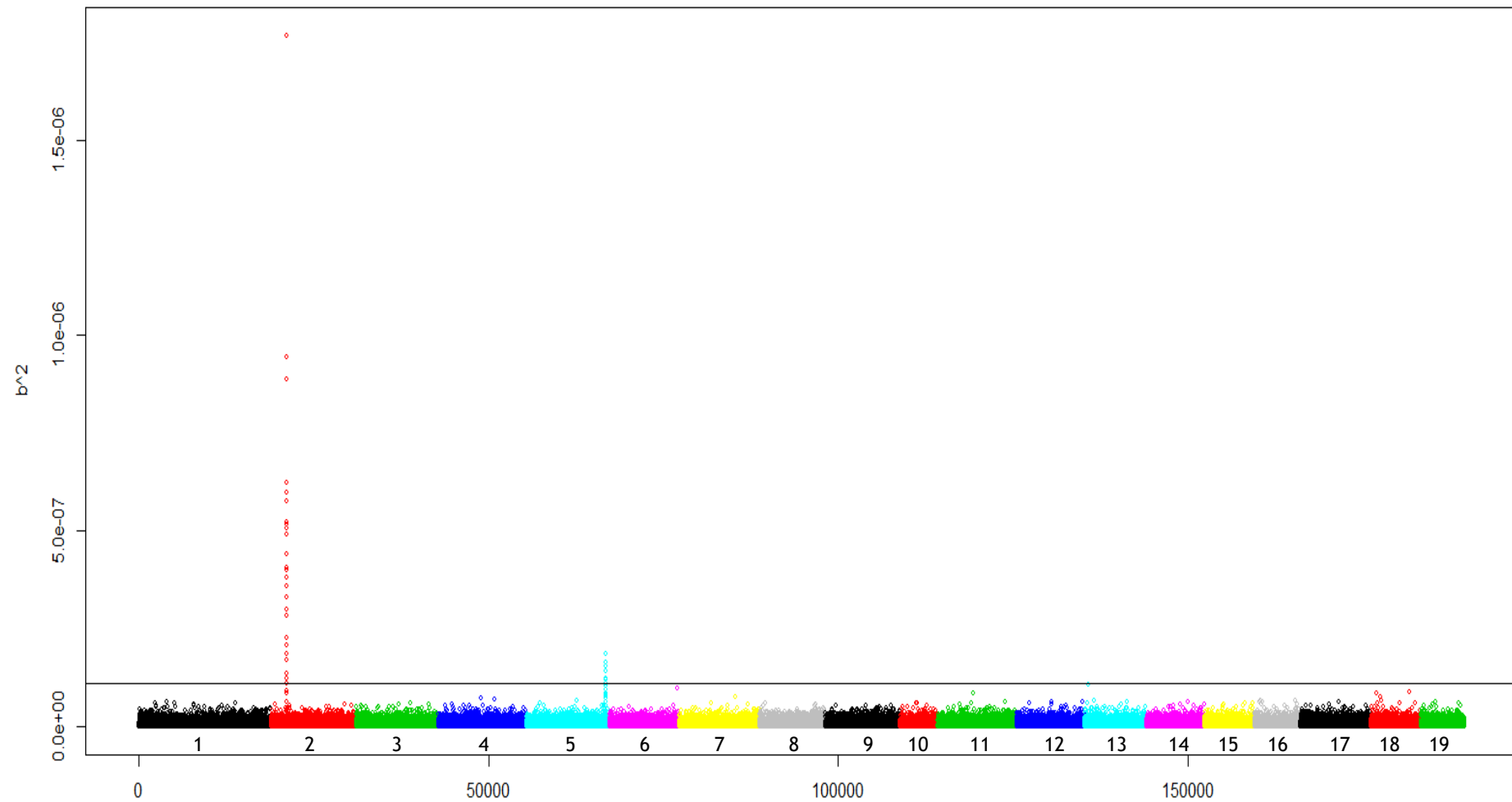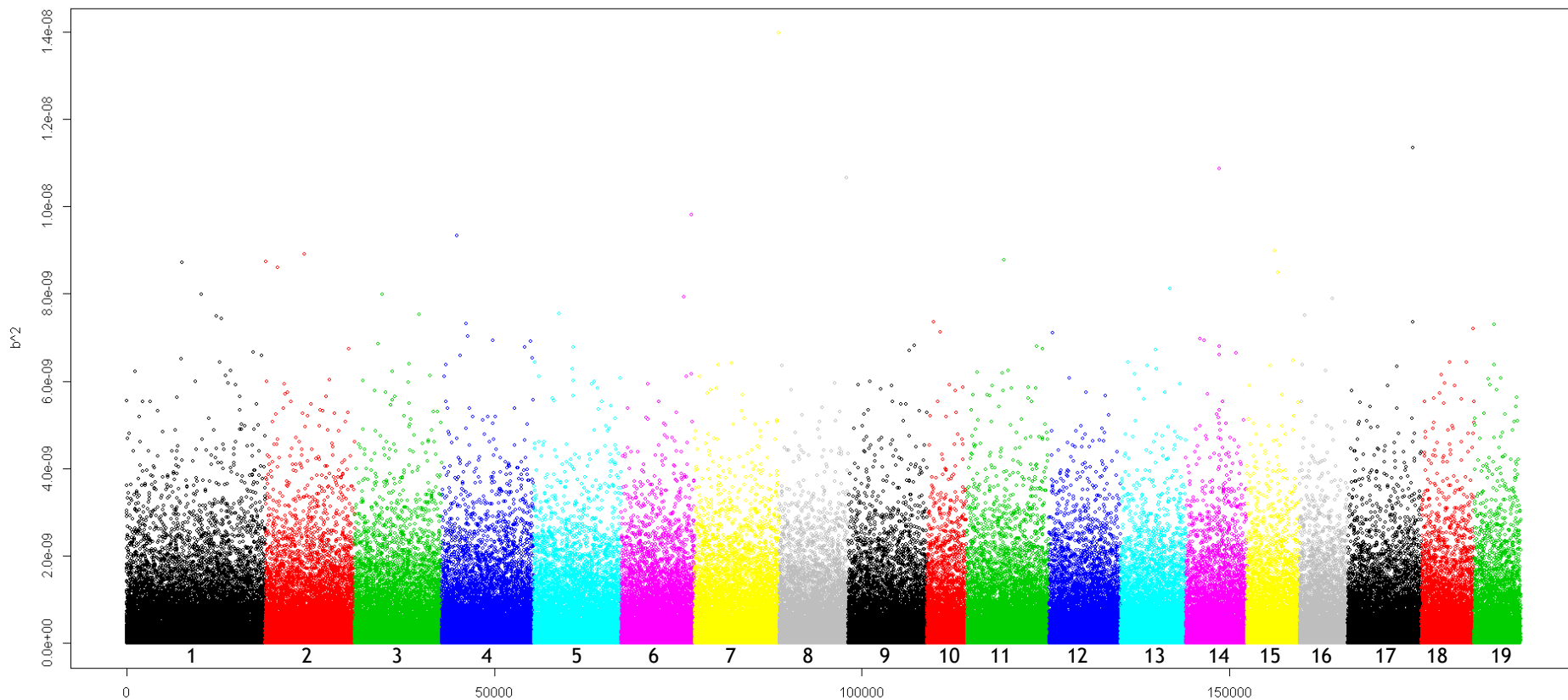
SelScan Program:

Gene-annotation enrichment and Functional annotation:

MEAN BIRTH WEIGTH

BIRTH WEIGTH STANDARD DEVIATION

Functional Cluster	Gene name	EnsemblID	Description	MUS
Cluster 1 (1.61)	*Acvr1c*	ENSMUSG00000026834	activin A receptor, type IC [Source:MGI Symbol;Acc:MGI:2661081]	2
	Acvr1	ENSMUSG00000026836	activin A receptor, type 1 [Source:MGI Symbol;Acc:MGI:87911]	2
	Eif2ak1	ENSMUSG00000029613	eukaryotic translation initiation factor 2 alpha kinase 1 [Source:MGI Symbol;Acc:MGI:1353448]	5
	Lmtk2	ENSMUSG00000038970	lemur tyrosine kinase 2 [Source:MGI Symbol;Acc:MGI:3036247]	5

BIOLOGICAL PROCESS

Acvr1c

- Response to stimulus
- Cell differentation
- Cell death
- Cell population proliferation
- Cellular component organization
- Establishment of localization
- Signaling
- Protein metabolic process

Acvr1

- Response to stimulus
- Cell differentation
- Cell death
- Signaling
- Protein metabolic process
- Nucleic acid-templated transcription
- System development

Eif2ak1

- Response to stimulus
- Homeostatic process
- Immune system process
- Cell differentation
- Cell population proliferation
- Establishment of localization
- Protein metabolic process
- System development

Lmtk2

- Response to stimulus
- Cell differentation
- Cellular component organization
- Establishment of localization
- Signaling
- Protein metabolic process
- System development

Immune system process	Cell process	Metabolic process	Developmental process

These preliminary results support the relationship between the trait MBW with robustness and animal welfare indicators

It still remains necessary to continue searching whether there are regions related to variability

However, further analysis is necessary to validate them. It is planned to genotype up to 1500 samples

Thanks for your attention

Monument to the Laboratory Mouse
Novosibirsk, Siberia (Rusia)

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